

-continued

<212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: sequence of PFN3A locus analyzed by
 pyrosequencing
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1) .. (53)
 <223> OTHER INFORMATION: Y is T or C

<400> SEQUENCE: 8

atgtaygtyg ygtgygttta ttagtattag gaggygygyg ggygtayggt tta

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We claim:

1. A method for identifying a sample as containing or not containing a vaginal epithelial cell, the method comprising the steps of:

(a) determining the level of methylation at SEQ ID NO: 2 in:

- i) a genetic material isolated from the sample, and
- ii) optionally, a control genetic material;

(b) optionally, obtaining one or more reference values corresponding to the level of methylation at SEQ ID NO: 2; and

(c) identifying the sample as:

- i) containing the vaginal epithelial cell based on the level of methylation of the cytosines at positions 33, 36, 38, 41, 61, 63, 65, 67, and 74 of SEQ ID NO: 2 in the genetic material isolated from the sample, or
- ii) not containing the vaginal epithelial cell based on the level of methylation of the cytosines at positions 33, 36, 38, 41, 61, 63, 65, 67, and 74 of SEQ ID NO: 2 in the genetic material isolated from the sample,

wherein the step of determining the level of methylation at SEQ ID NO: 2 comprises:

- (a) isolating the genetic material from the sample,
- (b) treating the isolated genetic material with bisulfite,
- (c) conducting a PCR using the bisulfite treated DNA as a template and a primer pair comprising a forward primer comprising SEQ ID NO: 3 and a reverse primer comprising SEQ ID NO: 4, and
- (d) analyzing the PCR amplicons produced in step (c) by pyrosequencing using a sequencing primer comprising the sequence of SEQ ID NO: 5.

2. The method of claim 1, characterized in that the control sample is obtained from one or more of the following: a known vaginal epithelial cell or a cell other than vaginal epithelial cell known to have methylation level at SEQ ID NO: 2 to be different from the methylation level at SEQ ID NO: 2 in the known vaginal epithelial cell.

3. The method of claim 2, characterized in that the cell other than vaginal epithelial cell is a buccal cell, a blood cell, or a sperm.

4. The method of claim 1, characterized in that the sample is a forensic sample.

5. The method of claim 1, characterized in that the sample is processed to separate a cell suspected to be the vaginal epithelial cell before step (a) of isolating the genetic material.

6. The method of claim 5, characterized in that the cell suspected to be the vaginal epithelial cell is isolated based on the cell being rich in glycogen compared to other cells in the sample.

7. A method for determining the level of methylation at the PFN3A locus in a genetic material from a cell, the method comprising the steps of:

- (a) isolating the genetic material from the cell,
- (b) treating the genetic material with bisulfite,
- (c) conducting a PCR using the bisulfite treated genetic material as a template and a primer pair comprising a forward primer comprising SEQ ID NO: 3 and a reverse primer comprising SEQ ID NO: 4, and
- (d) analyzing the PCR amplicons produced in step (c) by pyrosequencing using a sequencing primer comprising the sequence of SEQ ID NO: 5.

8. The method of claim 7, characterized in that the cell is isolated from a forensic sample.

9. The method of claim 8, characterized in that the cell isolated from the forensic sample is suspected to be a vaginal epithelial cell.

10. The method of claim 9, characterized in that the cell suspected to be the vaginal epithelial cell is isolated from the forensic sample based on the cell being rich in glycogen compared to other cells in the sample.

11. A kit comprising a forward primer comprising SEQ ID NO: 3 and a reverse primer comprising SEQ ID NO: 4.

12. The kit of claim 11, the kit further comprising a sequencing primer comprising SEQ ID NO: 5.

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